

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 07:39:00 ; Search time 25.94 Seconds
(without alignments)
3404.244 Million cell updates/sec

Title: US-08-153-397A-2

Sequence: 1 MGPEALSLILLLVASGDA.....QRPPSQLHRLAEADALNTV 919

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4881	99.0	913	2	receptor tyrosine
2	4656.5	94.5	876	2	protein-tyrosine k
3	4576.5	92.9	910	2	tyrosine kinase re
4	2404	48.8	855	2	protein-tyrosine k
5	2341	47.5	819	2	tyro 10 receptor k
6	1159	23.5	220	2	receptor tyrosine
7	969	19.5	791	2	hypothetical prote
8	963	19.5	248	2	receptor tyrosine
9	928.5	18.9	183	2	receptor tyrosine
10	648.5	13.2	821	1	brain-derived neur
11	648.5	13.2	821	1	brain-derived neur
12	648	13.1	818	1	brain-derived neur
13	645	13.1	818	1	brain-derived neur
14	641.5	13.0	825	2	brain-derived neur
15	640.5	13.0	825	2	brain-derived neur
16	628	12.7	799	1	brain-derived neur
17	624.5	12.7	825	1	brain-derived neur
18	623.5	12.7	839	1	brain-derived neur
19	615	12.5	503	4	brain-derived neur
20	613.5	12.4	803	4	brain-derived neur
21	608	12.3	282	2	brain-derived neur
22	608	12.3	806	2	brain-derived neur
23	604	12.3	852	2	brain-derived neur
24	597.5	12.1	946	1	brain-derived neur
25	597	12.1	737	2	brain-derived neur
26	590.5	12.0	605	2	brain-derived neur
27	590	12.0	871	1	brain-derived neur
28	588.5	11.9	881	1	brain-derived neur
29	584	11.9	685	1	brain-derived neur

30	576	11.7	981	1	FOATGM	gag-ab1 polyprotel
31	571	11.6	737	2	T31349	hypothetical prote
32	540.5	11.0	1363	2	T43320	insulin-like growt
33	537	10.9	937	2	A45082	neurotrophic recep
34	535.5	10.9	1382	1	INHUR	insulin receptor p
35	532.5	10.8	402	1	TYEVUR	insulin receptor p
36	531.5	10.8	1372	2	A34157	insulin receptor p
37	528.5	10.7	1383	2	A36080	insulin receptor p
38	523	10.6	1520	1	TVFPA	insulin receptor p
39	522.5	10.6	2338	2	T73957	insulin receptor p
40	522	10.6	2347	1	TVHURS	insulin receptor p
41	521.5	10.6	2311	1	TVCHSR	insulin receptor p
42	520	10.6	1123	2	A39962	insulin receptor p
43	518	10.5	2340	2	I48310	insulin receptor p
44	517	10.5	1130	1	TVHUA	insulin receptor p
45	517	10.5	1300	2	A36502	insulin receptor p

ALIGNMENTS

RESULT 1
A48280
receptor tyrosine kinase - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 24-Sep-1999
R:Johnson, J.D.; Edman, J.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 90: 5677-5681, 1993
A:Title: A receptor tyrosine kinase found in breast carcinoma cells has an extracell.
A:Reference number: A48280; MUID:93296201
A:Accession: A48280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-913 <RES>
A:Cross-references: GB:LI1315; NID:9403386; PID:AAA02866.1; PID:9403387
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino
C:Keywords: ATP
F:30-185/Domain: discoidin I amino-terminal homology <DNI>
F:608-912/Domain: protein kinase homology <KIN>
F:616-624/Region: protein kinase ATP-binding motif

Query Match	99.0%	Score 4881	DB 2	Length 913
Best Local Similarity	99.1%	Pred. No. 5.8e-214		
Matches 911	Conservative	2	Mismatches 0	Indels 6
Gaps				1
QY	1	MGPEALSLILLLVASGDA	DMKGFDPKCRVATLGMODRTIPDSDISASSMSDSTAR	60
DB	1	MGPEALSLILLLVASGDA	DMKGFDPKCRVATLGMODRTIPDSDISASSMSDSTAR	60
QY	61	HSRLSSDGDGACMPAGSVFPEKEEYLDQRLHLVAVYQGRHAGLGKEFRSRL	120	
DB	61	HSRLSSDGDGACMPAGSVFPEKEEYLDQRLHLVAVYQGRHAGLGKEFRSRL	120	
QY	121	RYSRDGRMGKMDWGOEIVISGNEDEGVYVLDKGPVATLFFYPRADVMSCVRY	180	
DB	121	RYSRDGRMGKMDWGOEIVISGNEDEGVYVLDKGPVATLFFYPRADVMSCVRY	180	
QY	181	ELYGLMRDGLISTYAPVQQTWYLSAVALNDSTYDGHVGGIYGGIQLADGVGDD	240	
DB	181	ELYGLMRDGLISTYAPVQQTWYLSAVALNDSTYDGHVGGIYGGIQLADGVGDD	240	
QY	241	FKRSQELRWPGDYVVGNSHSSFGYEMERFRLAFAQMYCHNNMTLGLARLFG	300	
DB	241	FKRSQELRWPGDYVVGNSHSSFGYEMERFRLAFAQMYCHNNMTLGLARLFG	300	
QY	301	VECRFRGPPAMAEGERPHNLGNIADPRAVSPPLGAVARPLQCRFLFAGPWILFS	360	
DB	301	VECRFRGPPAMAEGERPHNLGNIADPRAVSPPLGAVARPLQCRFLFAGPWILFS	360	
QY	361	EISFSDVYVNNSSPALGCTPPAPMPWPPPTNFSLSLEPRGOQPVAKAGSPAILI	420	
DB	361	EISFSDVYVNNSSPALGCTPPAPMPWPPPTNFSLSLEPRGOQPVAKAGSPAILI	420	

Db 361 EISFISDVYNNSSPALGCTFPAPMMPGPPPTNFSSLELEPRGQGVAKAESPTAII 420
QY 421 GCLVAIIILLIILALMLHRLSKAERLYEELTVHLSVPDITLINNRPGRE 480
Db 421 GCLVAIIILLIILALMLHRLSKAERLYEELTVHLSVPDITLINNRPGRE 480
QY 481 PPEYQERPRGNPPHSAFCVPSGALLSNPAYRLLATYARPPRGPPPTPAMAKPTNT 540
Db 481 PPEYQERPRGNPPHSAFCVPSGALLSNPAYRLLATYARPPRGPPPTPAMAKPTNT 540
QY 541 QASGDMEKEKPGAPLPPPPONSYPHYAEADIVTLQGTGNTYAVPALPGAVDGP 600
Db 541 QASGDMEKEKPGAPLPPPPONSYPHYAEADIVTLQGTGNTYAVPALPGAVDGP 600
QY 601 PRVDFPRSRIRFEKELGEGGFEVHLCEDVSPDLYSLDPLVNRKGPLLVAKILRPD 660
Db 601 PRVDFPRSRIRFEKELGEGGFEVHLCEDVSPDLYSLDPLVNRKGPLLVAKILRPD 660
QY 661 ATKNASESLESRNDFLEKVKIMSRLKDPNIRLLGVGVODDPLCMITDYMENGLNOFLS 720
Db 661 ATKNASESLESRNDFLEKVKIMSRLKDPNIRLLGVGVODDPLCMITDYMENGLNOFLS 720
QY 721 AHOLEDKAAGARDDGQAAGPTISYPMILHVAQAISGKRYLATLNFVRDLATRCCLY 780
Db 721 AHOLEDKAAGARDDGQAAGPTISYPMILHVAQAISGKRYLATLNFVRDLATRCCLY 780
QY 781 GENFTIKIADFGKSRNLYADYTRVQGRAVLPIRMMAECILMGKFTTASDVNAFGVTLM 840
Db 781 GENFTIKIADFGKSRNLYADYTRVQGRAVLPIRMMAECILMGKFTTASDVNAFGVTLM 840
QY 841 EVLMCRAQFGQLTDEQVYENAGEFFRDGRQVYLSRPACFOGLYEMLRCMSRESEQ 900
Db 841 EVLMCRAQFGQLTDEQVYENAGEFFRDGRQVYLSRPACFOGLYEMLRCMSRESEQ 900
QY 901 RPEFSQHLRFLAEDALNTV 919
Db 901 RPEFSQHLRFLAEDALNTV 919
QY 901 RPEFSQHLRFLAEDALNTV 919
Db 901 RPEFSQHLRFLAEDALNTV 919

RESULT 2

A:Accession: A49508
protein-tyrosine kinase (EC 2.7.1.112) trkE precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C:Accession: A49508; 138358; 537402
R:J. Marco, E. Cutilli, N.; Guerra, L.; Cancedda, R.; De Luca, M.
J. Biol. Chem. 268, 24290-24295, 1993
A:Title: Molecular cloning of trkE, a novel trk-related putative tyrosine kinase receptor
A:Reference number: A49508; M0ID:94043265
A:Accession: A49508
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-876 <DIA>
A:Cross-references: EMBL:X74979; NID:g400462; PIDN:CAA52915.1; PID:g400463
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:30-185/Domain: discoidin I amino-terminal homology <DNI>
F:571-875/Domain: protein kinase homology <KIN>
F:579-587/Region: protein kinase ATP-binding motif

Query Match 94.5%; Score 4656.5; DB 2; Length 876;
Best Local Similarity 95.3%; Pred. No. 8.1e-204;
Matches 876; Conservative 0; Mismatches 0; Indels 43; Gaps 2;

QY 1 MGPEALSSLLILLVAVSGADMGHFDPAKCRALMGKRTIPDSISASSSSDSTAAR 60
Db 1 MGPEALSSLLILLVAVSGADMGHFDPAKCRALMGKRTIPDSISASSSSDSTAAR 60
QY 61 HSRLESSDGDGAMCPAGSYFPKKEEYLOVDLQRLHLVALVGTGRRAGGAGKEFSRYR 120
Db 61 HSRLESSDGDGAMCPAGSYFPKKEEYLOVDLQRLHLVALVGTGRRAGGAGKEFSRYR 120

QY 121 RYSRDGRMMGMDRMGOEYISGNEDEGVYLDLGPMTYARLYREYPRADRVMSCLRY 180
Db 121 RYSRDGRMMGMDRMGOEYISGNEDEGVYLDLGPMTYARLYREYPRADRVMSCLRY 180
QY 181 ELYGCLMRDGLSTYAVGOTMYLSEAVYLNDSYDGHVIGLOYGGLQGLADGVGLD 240
Db 181 ELYGCLMRDGLSTYAVGOTMYLSEAVYLNDSYDGHVIGLOYGGLQGLADGVGLD 240
QY 241 FRKSOELRVMPGYDYVMSHNSFSGVEMEFEEDRLRAQAMVHONNNHTGALRPG 300
Db 241 FRKSOELRVMPGYDYVMSHNSFSGVEMEFEEDRLRAQAMVHONNNHTGALRPG 300
QY 301 VECFRFRGPMAMGEEMRNLGNLDPARAASVYLGRVAFLOCREFLAGPMLIFS 360
Db 301 VECFRFRGPMAMGEEMRNLGNLDPARAASVYLGRVAFLOCREFLAGPMLIFS 360
QY 361 EISFISDVYNNSSPALGCTFPAPMMPGPPPTNFSSLELEPRGQGVAKAESPTAII 420
Db 361 EISFISDVYNNSSPALGCTFPAPMMPGPPPTNFSSLELEPRGQGVAKAESPTAII 420
QY 421 GCLVAIIILLIILALMLHRLSKAERLYEELTVHLSVPDITLINNRPGRE 480
Db 421 GCLVAIIILLIILALMLHRLSKAERLYEELTVHLSVPDITLINNRPGRE 480
QY 481 PPEYQERPRGNPPHSAFCVPSGALLSNPAYRLLATYARPPRGPPPTPAMAKPTNT 540
Db 481 PPEYQERPRGNPPHSAFCVPSGALLSNPAYRLLATYARPPRGPPPTPAMAKPTNT 540
QY 541 QASGDMEKEKPGAPLPPPPONSYPHYAEADIVTLQGTGNTYAVPALPGAVDGP 600
Db 541 QASGDMEKEKPGAPLPPPPONSYPHYAEADIVTLQGTGNTYAVPALPGAVDGP 600
QY 601 PRVDFPRSRIRFEKELGEGGFEVHLCEDVSPDLYSLDPLVNRKGPLLVAKILRPD 660
Db 601 PRVDFPRSRIRFEKELGEGGFEVHLCEDVSPDLYSLDPLVNRKGPLLVAKILRPD 660
QY 661 ATKNASESLESRNDFLEKVKIMSRLKDPNIRLLGVGVODDPLCMITDYMENGLNOFLS 720
Db 661 ATKNASESLESRNDFLEKVKIMSRLKDPNIRLLGVGVODDPLCMITDYMENGLNOFLS 720
QY 721 AHOLEDKAAGARDDGQAAGPTISYPMILHVAQAISGKRYLATLNFVRDLATRCCLY 780
Db 721 AHOLEDKAAGARDDGQAAGPTISYPMILHVAQAISGKRYLATLNFVRDLATRCCLY 780
QY 781 GENFTIKIADFGKSRNLYADYTRVQGRAVLPIRMMAECILMGKFTTASDVNAFGVTLM 840
Db 781 GENFTIKIADFGKSRNLYADYTRVQGRAVLPIRMMAECILMGKFTTASDVNAFGVTLM 840
QY 841 EVLMCRAQFGQLTDEQVYENAGEFFRDGRQVYLSRPACFOGLYEMLRCMSRESEQ 900
Db 841 EVLMCRAQFGQLTDEQVYENAGEFFRDGRQVYLSRPACFOGLYEMLRCMSRESEQ 900
QY 901 RPEFSQHLRFLAEDALNTV 919
Db 901 RPEFSQHLRFLAEDALNTV 919
QY 901 RPEFSQHLRFLAEDALNTV 919
Db 901 RPEFSQHLRFLAEDALNTV 919

RESULT 3

A:Accession: A53137
Tyrosine kinase receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A53137
R:Sanchez, M.P.; Tapley, P.; Saini, S.S.; He, B.; Pulido, D.; Barbacid, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 1819-1823, 1994
A:Title: Multiple tyrosine protein kinases in rat hippocampal neurons: Isolation of p
A:Reference number: A53137; M0ID:94173920
A:Accession: A53137
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-910 <RES>
A:Cross-references: GB:L26525; NID:g432480; PIDN:AAA21089.1; PID:g432481
C:Genetics:

A, Gene: Pck-3
C, Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C, Keywords: ATP
F:31-186/Domain: discoidin I amino-terminal homology <DNI>
F:605-909/Domain: protein kinase homology <KIN>
F:613-621/Region: protein kinase ATP-binding motif

Query Match 92.9%; Score 4576.5; DB 2; Length 910;
Best Local Similarity 93.0%; Pred. No. 3.5e-200;
Matches 856; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

1 MGPALSS-LLILLVYASGDADKMGHFDPAKCRATLGMODRTIPDSISASSWSGSTAA 59
1 MGTGLSSLLILLVYASGDADKMGHFDPAKCRATLGMODRTIPDSISASSWSGSTAA 60
60 RHRLSSSDGAGMCPAGSVFPEEYLOVDLRLHLVALVGTGRRHAGLGKESRSYR 119
61 RHRLSSSDGAGMCPAGSVFPEEYLOVDLRLHLVALVGTGRRHAGLGKESRSYR 120
120 LRSRSDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 179
121 LRSRSDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 180
180 VELYGLMDGLSTYAPVQOTWYISEAVYLYNDSTYDGHVGTGGLQGLADGVVGLD 239
181 VELYGLMDGLSTYAPVQOTWYISEAVYLYNDSTYDGHVGTGGLQGLADGVVGLD 240
240 DRRKSOELRWPGDYVYGNSSHSFSGYVMEFEFRLRAFOAMOVHNNMTLGARLP 239
241 DRRKSOELRWPGDYVYGNSSHSFSGYVMEFEFRLRAFOAMOVHNNMTLGARLP 300
300 GVECRRRGPAAWMEGEPHNLGNLGPRAAVSVPLGGRVAPRLQCFLEAGPWL 359
301 GVECRRRGPAAWMEGEPHNLGNLGPRAAVSVPLGGRVAPRLQCFLEAGPWL 360
360 SEISFISDVVNSSPALGTFPPAPMPPGPPTNFSLELEPRGQPVAKAGSPATL 419
361 SEISFISDVVNSSPALGTFPPAPMPPGPPTNFSLELEPRGQPVAKAGSPATL 416
420 TCGLVAVIILLIILALMLRHLRRLSKAERVLEELVYHLSVPGDTILINNRPGR 479
421 TCGLVAVIILLIILALMLRHLRRLSKAERVLEELVYHLSVPGDTILINNRPGR 476
480 EPPPOEPRRGNPNSAPCVNGSALLSNPARYLLLTATYARPPGPPPPAKKPTN 539
477 EPPPOEPRRGNPNSAPCVNGSALLSNPARYLLLTATYARPPGPPPPAKKPTN 536
540 TQVAGSDYMEPEKPGAPLPPPPONSVPYAEADIVTLQGVYGGNTYAVAPALPGAVPG 599
537 TQVAGSDYMEPEKPGAPLPPPPONSVPYAEADIVTLQGVYGGNTYAVAPALPGAVPG 596
600 PRRVDPNRSRLRFEKELGEGFGEVHLCEVDSPODLVSLDFPLNARKGHPLLVAVKILRP 659
597 PRRVDPNRSRLRFEKELGEGFGEVHLCEVDSPODLVSLDFPLNARKGHPLLVAVKILRP 656
660 DATKAASSLFRNDELKVKIMSLKPNITRLLGVCYQDDPLCMTITTYMENGDIQPL 719
657 DATKAASSLFRNDELKVKIMSLKPNITRLLGVCYQDDPLCMTITTYMENGDIQPL 710
720 SAHOLEDRKAAGAGDGOAAGPTISYPMLLHVAQAQIASGMRYLATLNVHDLATRNCL 779
721 SAHOLEDRKAAGAGDGOAAGPTISYPMLLHVAQAQIASGMRYLATLNVHDLATRNCL 770
780 VGENTTIIRIADFGMSRNLVAGDYVVOGRAVLPIRMMAECILMGKFTTASDVMAFGVTL 839
771 VGENTTIIRIADFGMSRNLVAGDYVVOGRAVLPIRMMAECILMGKFTTASDVMAFGVTL 830
840 MEVLMLCAOPRGOLTDGOVLENAGEFFRDGROYVLSRPACPGGLYVLMRCSRSSE 899
831 MEVLMLCAOPRGOLTDGOVLENAGEFFRDGROYVLSRPACPGGLYVLMRCSRSSE 890
900 QRPFSQHLRLAEDALNTV 919

891 QRPFSQHLRLAEDALNTV 910

RESULT 4
542621

protein-tyrosine kinase (EC 2.7.1.112) - human

C, Species: Homo sapiens (man)

C, Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999

C, Accession: 542621

R, Kern, T.; Holtrich, U.; Braeuninger, A.; Boehme, B.; Wolf, G.; Ruebsaamen-Walzgmann, Oncogene 8, 3433-3440, 1993

A, Title: Structure, expression and chromosomal mapping of TRK from man and mouse: a

A, Reference number: 542621; M0ID: 94067796

A, Accession: 542621

A, Molecule type: mRNA

A, Residues: 1-855 <KAR>

A, Cross-references: EMBL: X74764; NID: g433337; PIDN: CA52777.1; PID: g433338

C, Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino

C, Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F:29-185/Domain: discoidin I amino-terminal homology <DNI>

F:561-855/Domain: protein kinase homology <KIN>

F:569-577/Region: protein kinase ATP-binding motif

Query Match 48.8%; Score 2404; DB 2; Length 855;
Best Local Similarity 51.8%; Pred. No. 6.8e-102;
Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

3 PEALSSILLILLVYASGDADKMGHFDPAKCRATLGMODRTIPDSISASSWSGSTAARS 62
5 PRLVLEFLLPLTIS--SAKAQVNPALICRYPGMGGQIPDDITASSQWSESTAKXG 61
63 RLESSDGDGAMCPAGSVFPEEYLOVDLRLHLVALVGTGRRHAGLGKESRSYR 121
62 RLESSDGDGAMCPAGSVFPEEYLOVDLRLHLVALVGTGRRHAGLGKESRSYR 121
122 YSRDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 181
122 YSRDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 181
182 YSGDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 181
182 YSGDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 239
182 YSGDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 239
182 YSGDGRMGKMDKMGQVITSGNDEPQVYAKDLGPRVAVARVRYPRADRYMSYCLR 240
240 DRRKSOELRWPGDYVYGNSSHSFSGYVMEFEFRLRAFOAMOVHNNMTLGARLP 299
241 DRRKSOELRWPGDYVYGNSSHSFSGYVMEFEFRLRAFOAMOVHNNMTLGARLP 300
300 GVECRRRGPAAWMEGEPHNLGNLGPRAAVSVPLGGRVAPRLQCFLEAGPWL 359
301 GVECRRRGPAAWMEGEPHNLGNLGPRAAVSVPLGGRVAPRLQCFLEAGPWL 359
360 SEISFISDVVNSSPALGTFPPAPMPPGPPTNFSLELEPRGQPVAKAGSPATL 418
360 SEISFISDVVNSSPALGTFPPAPMPPGPPTNFSLELEPRGQPVAKAGSPATL 418
360 SEISFISDVVNSSPALGTFPPAPMPPGPPTNFSLELEPRGQPVAKAGSPATL 400
419 TCGLVAVIILLIILALMLRHLRRLSKAERVLEELVYHLSVPGDTILINNRPGR 476
401 TCGLVAVIILLIILALMLRHLRRLSKAERVLEELVYHLSVPGDTILINNRPGR 460
477 GPREP-----PPYQEPNPNPNSAPCVNGSALLSNPARYLLLTATYAR 523
461 SPESGNSNTYDRIPLRDYQEP-----SLIKRLPEF----- 494
524 PRGPPPPAKKPTNTQVYSGDYMEPEKPGAPLPPPPONSVPYAEADIVTLQGVYGG 583
495 -----APGEESGCGVYKVPVQSGP-----EGVPHYAADIVNLQGVYGG 535
584 NTYAVAPALPGAVGDPNPPV-DPPRSRLRFEKELGEGFGEVHLCEVDSPODLVSLDFPL 642
536 NTYAVAPALPGAVGDPNPPV-DPPRSRLRFEKELGEGFGEVHLCEVDSPODLVSLDFPL 595

QY 643 NVKRGHPLLVAVKILRPATKNASPSLESRNDFLKEVKINRSLKDPNITILLGCVQDDP 702
 Db 536 DVSANQPLVAVKMLRPADKNRA-----RNDPLKEIKIMSRKLDPNITILLGCVQDDP 649
 QY 703 LCMITDVENGDINOFLSAHOLEDKAAGPAGDQAAGPISYPMILHVAQAASGRY 762
 Db 650 LCMITEVENGDINOFLSRHE-----PPNSSSDVRTVSTNLEKMTQIASGMY 700
 QY 763 LATINFEVARDLATRNCILGVEENFTIKIADFGMSRLIAGDYRVQRAVLPIRMAMECIL 822
 Db 701 LSLINFEVARDLATRNCILGKNTTIKIDFGMSRLISGDIYRIGRAVLPIRMAMECIL 760
 QY 823 MGFRTASDVAFVGYTLMEVLMCRAPFGQLTDOVIENAGFEPRDGRQVILSRPAC 882
 Db 761 LKFTTASDVAFVGYTLMEVLMCRAPFGQLTDOVIENAGFEPRDGRQVILSRPAC 820
 QY 883 POGLEYELMRCMSRESEORPPFSOLHRLAE 913
 Db 821 PDSYKMLSCMRDRTKNRPSFOETHILLLO 851

RESULT 5

tyro 10 receptor kinase - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence,revision 02-Jul-1996 #text_change 24-Sep-1999
 C:Accession: I48859; S42796
 Ri1at, C.; Lemke, G.
 Oncogene 9, 877-883, 1994
 A:Title: Structure and expression of the Tyro 10 receptor tyrosine kinase.
 A:Reference number: I48859; M01D:94151011
 A:Accession: I48859
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-819 <RES>
 A:Cross-references: EMBL:X76505; NID:9435161; PIDN:CAA54040.1; PID:9435162
 C:Genetics:
 A:Gene: tyro 10
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: Arp
 F:526-819/Domain: protein kinase ATP-binding motif
 F:534-542/Region: protein kinase ATP-binding motif

Query Match 47.5%; Score 2341; DB 2; Length 819;
 Best Local Similarity 52.1%; Pred. No. 46e-99;
 Matches 465; Conservative 116; Mismatches 208; Indels 104; Gaps 15;

QY 42 IPDSDISASSWSSTARSHSLSSSDGAMCPAGSVFPE-BEYLQVLDQLRLHVALV 100
 Db 6 IPDEDITASSQMSSTAKYGRSLSEBDGAMCPDPIYQPDLEKFIQIDRLHFTLV 65
 QY 101 GTGRRHAGGCKEFSRSLRLKYSRDRRMKMKRMGOEYISGNEDEBGVYLKLGPPMV 160
 Db 66 GTGRRHAGGCKEFSRSLRLKYSRDRRMKMKRMGOEYISGNEDEBGVYLKLGPPMV 125
 QY 161 ARLVFEYRARRVAVSVCLRLVELYGLMRDGLSTAPVQGMPL--SEAVLYLNDSTYDGH 218
 Db 126 ARFRLRLPYVDHSMNVCMCRVELYGCWLDGLVSTNAPAGQGFVLPQGSITILLNDSTYDGH 184
 QY 219 TVGGLQVGGGLQGLADGVVGLDDFRKSOELRWPGDYVGVSNHSSFGSYVEEPEFRLR 278
 Db 185 AVGSMTSEGGLQGLDGVSGLDLDFQTHYHYWPGDYVGVSNHSSFGSYVEEPEFRLR 244
 QY 279 AFQAMOVCHCNMHTLGLARLPBGVCCRFRGPMAMEGEPRRHNLGMLGDPRAAAYVPL 338
 Db 245 NPTTKAHCHCNMHTLGLARLPBGVCCRFRGPMAMEGEPRRHNLGMLGDPRAAAYVPL 303
 QY 339 GGRVAFRLQCFRLFAGPMLIFSEISFISD--VYVNSSPALGCTPPAPMPPPGPTNFS 396
 Db 304 HHRVAAIKQCYHFRADYMMSESEITFOSDAMYNNS-----GALPTP----- 346
 QY 397 SLELEPRGQGPVAKESPTAILIGCLVAITILLITLMLWRLHWRLLSKAERYLE 456

Db 347 --NAPTYDPMELKYDSDNTRILLIGCLVAITILLITLMLWRLHWRLLSKAERYLE 403
 QY 457 EELFVHLSVPGDITLINNR-----GPRRP-----PPYOEPRRGPRPSACVP 501
 Db 404 DEMTVSLSLPSESSMFNNRSSSPSEDSNSTYRIRPELRDYOEP----- 449
 QY 502 NGSALLSNPARYRLLLATYARPGRPGPPRPMKPTNQASGDYMEPEKPGAPLPP 561
 Db 450 --SRILKRLPEF-----APGEEEGCGGVKPAQPNP----- 480
 QY 562 PONSVPYHAEADIVTLOGVTGNTYAVPALPGAVGGPPRY-DEPRSLRFRKEKLEGO 620
 Db 481 --EGVPHYAEADIVNLOGVTGNTYAVPALMDLSCGVAVEEFPRLIAFKKELGEG 538
 QY 621 FGEVHLCEVSDPOLVSLDFPLNVRKGPPLVAKILRPDRTKASLSFRNPFLEVK 680
 Db 539 FGEVHLCEVSDPOLVSLDFPLNVRKGPPLVAKILRPDRTKASLSFRNPFLEVK 592
 QY 681 IMSRLKDPNITIRLLGVCVQDDPLCMITDYEMNGDINOFLSAHOLEDKAAGPAGDQAQ 740
 Db 593 IMSRLKDPNITIRLLAVCTEDPLCMITEYEMNGDINOFLSRHEPLSSCSDA----- 644
 QY 741 GPRTISYPMILHVAQAASGRMYLATLNFVHRDLATRNCILGVEENFTIKIADFGMSRLIAG 800
 Db 645 --TVSYANKLFMAQIASGMYLSSLNFVHRDLATRNCILGKNTTIKIDFGMSRLIAG 702
 QY 801 DYRYVOGRAVLPITMMAMECLIMKFTTASDVAFVGYTLMEVLMCRAPFGQLTDOVI 860
 Db 703 DYRIQGRAVLPITMMAMECLIMKFTTASDVAFVGYTLMEVLMCRAPFGQLTDOVI 762
 QY 861 ENAGEFFRDGRQVILSRPACPOGLEYELMRCMSRESEORPPFSOLHRLAE 913
 Db 763 ENTGEFFRDGRQVILSRPACPOGLEYELMRCMSRESEORPPFSOLHRLAE 815

RESULT 6

receptor tyrosine kinase - rat (fragment)
 C:Species: Rattus sp. (rat)
 C:Date: 02-Aug-1996 #sequence,revision 02-Aug-1996 #text_change 24-Sep-1999
 C:Accession: I80329
 R:Sakuma, S.; Saya, H.; Iijichi, A.; Tojilon, P.J.
 Radiat. Res. 143, 1-7, 1995
 A:Title: Radiation induction of the receptor tyrosine kinase gene Ptk-3 in normal rat
 A:Reference number: I59442; M01D:95320273
 A:Accession: I80329
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-220 <RES>
 A:Cross-references: GB:S77585; NID:9573332; PIDN:AAB34728.1; PID:9573333
 C:Genetics:
 A:Gene: Ptk-3l
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 23.5%; Score 1159; DB 2; Length 220;
 Best Local Similarity 98.6%; Pred. No. 4e-46;
 Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 404 GQGFVAKAESPTAILIGCLVAITILLITLMLWRLHWRLLSKAERYLEELVHL 463
 Db 1 GQGFVAKAESPTAILIGCLVAITILLITLMLWRLHWRLLSKAERYLEELVHL 60
 QY 464 SVPGDITLINNRGPRPPYOEPRRGNDPHSAPCVNSALLSNPAYRLLATYARP 523
 Db 61 SVPGDITLINNRGPRPPYOEPRRGNDPHSAPCVNSALLSNPAYRLLATYARP 120
 QY 524 PRGGRPTPMAKPTNQASGDYMEPEKPGAPLPPRPNVPHYAEADIVTLOGVTG 583
 Db 121 PRGGRPTPMAKPTNQASGDYMEPEKPGAPLPPRPNVPHYAEADIVTLOGVTG 180
 QY 584 NTYAVPALPGAVDGPDPVDFPRSRRLFRKEKLEGGQFGE 623

Db 181 NTYAVPALPGAVGDGPPRVDFPERSRLFKKELGEGGGE 220

RESULT 7

hypothetical protein F11D5.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
 C:Accession: T16031

R:Name, M.

submitted to the EMBL Data Library; November 1995

A:Description: The sequence of *C. elegans* cosmid F11D5.

A:Reference number: 218449

A:Accession: T16031

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-791 <NHA>

A:Cross-references: EMBL:U01532; NID:g1118032; PID:g1118035; PIDN:AAA83276.1; CESP:F11D5

A:Gene: CESP:F11D5.3

A:Introns: 52/2; 85/1; 129/3; 179/1; 275/3; 380/1; 469/2; 493/2; 569/1; 612/2; 638/2; 74

C:superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 19.7%; Score 969; DB 2; Length 791;

Best Local Similarity 28.3%; Pred. No. 5.5e-37;

Matches 254; Conservative 150; Mismatches 310; Indels 184; Gaps 31;

46 DISASSSSMSDSTAR-HSRLESSDGDGACPGSVFPKEEYLVQDRLHLVALYGTG 104

34 DLNMLGKMFNGNSPEIRFTAHQESGACPKNINSLSKMLDISVDTVITSVETG 93

105 RAAGGJGKESRSYRLRYSDG--RRMGKMDRGQEVISGNEDEGVYLRKLPYVAVL 163

94 RPDGGRMEYATFAKIOYMRPLNANASYSKDDFELTIPANNDETHAIRHLDAIARR 153

164 VREYPRADRVAGYCLARELYGCLMBGLLSTYAPVGTMTLSEAVYLYNDSTYDGHYVGL 223

154 IRVTPNSNRTYCMRYEVGCPDSDLVFYNDQGD--LQSGISYHDSYDNLNSP 210

224 QY-GGLGQLADGVYGLDDFKSSELRYWPGYDYVGNHSGYVMEFEFDRALFAQA 282

211 HLTGGIGKLYDGEVKNVNVN-----HKVVGMRK--RGNVYLAPEFSELRNIGS 261

283 MGVHCNMHTLGLRPLGVECRFRGPGAMAMEGEPMRHNLG-----NLGDP-- 330

262 ILHTSN-----EFKKS-AKAFSSATVLFESINGKDESDTIYHNNPDETES 306

331 --ARAASVPLGVRVAFLOCRFLFA--GPWLLSEISFISDVN-----NSSPALGTFPP 382

307 EYPRWIRIVNNHIAKIRLNFQDSWLFISEVNFESNMHNIELNDVYI----- 360

383 APMWPPGPPTNFSSLELPRGQOPAKAEGSPALIGLVAIIILLLIILMLRLH 442

361 -----PDSVSYFSTHDDGT-----SMFAFI--FFMELIVAVIILTVLRKR 403

443 WRRLLS-----KAERYVLEELTVHLVSPGDTLLNNRPGPREPPYOEPGRGNPHSA 497

404 EYRVKASSPSNAKKEIL-----LTIDGNTIKHH-----VPSITYQVNR----- 442

498 PCVPNGSALLSNPAVRLATYARPPRGPPPTPAMAKPTN---QANSQDMEPEKPG 554

443 ---DNLQNLLEKMPSPITISDAEDISVCSQDVTA---NPLLYGIDGPY-DTQKRS 493

555 ADLPPPPONSYPVHAADIVTLQGTGNTYAVPALPGAVGDDGPRVDFPERSRLRFE 614

494 NPL-----SSWVKYSY-----GEVYCT-TLP-----EIAKDILCVS 555

615 KLGEQGFQVHLCEVDSPODLVSLDFPLNVRKGHPLVAVKTLRPDANASFSLSRND 674

526 RIGGEGFEVDLCOLEN-----RK-----VAVKKLH-----GISQADERS 560

QY 675 ELKEVKINSRLKDPNIIIRLLGVCVODDPLCMITDYMENGDLNOFLSAQLEDKAEGAPG 734

Db 561 FHRIRVLSLKHPNVVEYVGVCTIOKPIICIMETMENGDLKSYI----- 605

QY 735 DQAAOGPTISYPMILHVAQAQASGMRYLATNFRHDLATRNCLVGENFTIKINDSOMS 794

Db 606 ---LKNPTIOTSQCTISICTOLAAGIAYLESCNPFVHRDIAARNCLVDEGNVKIADFGMA 661

QY 795 RNLVADYRYVQGRAVLPIRMAMECILMGKPTASDVWAGVYTWMEYLMICRAQPGOL 854

Db 662 RSLYQGYEYKVGKRVLPPIRMAMAILLKRTSDVWAGVYTWMEYLSLSEKPYSDM 721

QY 855 TDEOYIENAGEEERDQGRQVYLRPPACPGYLR--ELMLRCSRESQRPFSOLHRL 911

Db 722 TDDVYENLQMSSTGSLKQVLSRPMCPKLYNQIILPCNNYESRRPSENVNHL 779

RESULT 8

receptor tyrosine kinase Xtk - African clawed frog (fragment)
 C:Species: *Xenopus laevis* (African clawed frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 10-Sep-1997
 C:Accession: A44547

R:Name, Z.

submitted to the Protein Sequence Database, December 1993

A:Reference number: A44547

A:Accession: A44547

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-248 <KEL>

C:superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

F:1-246/Domain: protein kinase homology (fragment) <KIN>

Query Match 19.5%; Score 963; DB 2; Length 248;

Best Local Similarity 72.6%; Pred. No. 3.3e-37;

Matches 175; Conservative 28; Mismatches 32; Indels 6; Gaps 1;

668 SLFRSNDLKEVKIKMSRLKDPNIIIRLLGVCVODDPLCMITDYMENGDLNOFLSAQLEDK 727

Db 2 SLINSDFLKEKILSLSDPHIIRLLGACLEDPLCMITDYMENGDLNOFLSHHDEG 61

QY 728 AAEAPDGGQAAGPTISYPMILHVAQAQASGMRYLATNFRHDLATRNCLVGENFTIK 787

Db 62 EENG-----AHCPLAISYSLHLVALQISGMKYLSSLNFRHDLASRNCLVGENFTIK 115

QY 788 IADFGSRNLYAGGYRVOGRAVLPPIRMAMECILMGKPTASDVWAGVYTWMEYLMICR 847

Db 116 IADGSRNLYAGGYRVOGRAVLPPIRMAMECILMGKPTASDVWAGVYTWMEYLMICR 175

QY 848 AOPFGQLTDEOYIENAGEEERDQGRQVYLRPPACPGYLR--ELMLRCSRESQRPFSOL 907

Db 176 EQPYGELSDDEDYIENAGEIRDSKKQIFLRPPCPQPLTELMQCSRDCKRPPSPQDI 235

QY 908 H 908

Db 236 H 236

RESULT 9

159442

receptor tyrosine kinase - rat (fragment)

C:Species: *Rattus sp.* (rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999

C:Accession: I59442

R:Sakuma, S.; Seta, H.; Tjich, A.; Tofilon, P.J.

R:Title: Radiation induction of the receptor tyrosine kinase gene Ptk-3 in normal rat

A:Reference number: I59442; MID:95320273

A:Accession: I59442

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-183 <RES>

F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK2>
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK3>
 F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK3>
 F:435-451/Domain: transmembrane status predicted <TM>
 F:452-821/Domain: cytosolic status predicted <CYT>
 F:535-813/Domain: protein kinase homology <KIN>
 F:543-551/Region: protein kinase ATP-binding motif
 F:571/Active site: Lys #status predicted
 F:705/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F:816/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 13.2%; Score 648.5; DB 1; Length 821;
 Best Local Similarity 30.1%; Pred. No. 1.8e-22;
 Matches 201; Conservative 72; Mismatches 188; Indels 207; Gaps 23;

QY 373 SPALGTPPPAPWPPPPPTNSSLEPRGOOPVAKAGSPFALLIGLVAIILLLL 432
 DB 217 SCVSGDDPLTTLTYDVGNLVSKHNNSTHOGSLRITNISDDSGKISCY----- 267
 QY 433 IALMLRLHWRLLSKAERVLVEELIYHLSV---PGDTILLNNRGPPEPP----- 482
 DB 268 -----AENLVGEDDDSVNLTVHFAPTITFL-----ESPSTDHHC 302
 QY 483 -PYOEBPRGNPPSPAPCVNGS-----ALLSNPA-----Y 513
 DB 303 IFF---TVGNPKPRALOWPFGNAILNESKICIKIHVTNTEYHGLQLOLPHMANNQDY 359
 QY 514 RLIL-----ATYARPPRGPPPTPAMAKPTNTQAYSQDMEP--E 551
 DB 360 TLMAKNKYGKDEROISAHFNGRPGVDYETNPNTPEVLIEDWTPTDI---GDTTKNSE 415
 QY 552 KGGAPLPPPPQSVHYAEADIVTQGV----- 580
 DB 416 ISTDVADOTNRHLSVAVVAVSVAGCCLVMLLLKLARSKGKMGKPAVYSNDD 475
 QY 581 -----TGNNTYAVPALPGAVGDP--PRVDFP-----RS 608
 DB 476 SASPLHINSNTPTSSSGGPRAVIIGMTKIVYENPOFGITNSOLKPDIVQHTKRH 535
 QY 609 RLRFKKLEGGQGEVHLC---VDSPODVLSDPFLNVRKGPLLVAVKILRPDATTNA 665
 DB 536 NIVLKRLEGGAFKVFLEACVYLCEPD-----KILVAVYTKL-DASDNA 580
 QY 666 SRSLSRNFLEKVKIMSLKDPNIRLLGVCYQDDPLCMITDYMEGDIQGLSAHQLE 755
 DB 581 -----KQFHRHAEELLTMOHEHIVKFGVCVEGDPILMVEFYMKHGDLNKLRAHGP 634
 QY 726 D-KAAGAPGDDQAAGPT-ISTYPMILHYAAQIASGMRYLATLNFVHRDLATRNCLVGEN 783
 DB 635 AYLMAGNP-----PELITQOSMLHTAQOIAAGMYILASQHFVHRDLATRNCLVGEN 666
 QY 784 FTIKIADFGMSNLVAGDYRYVQRAVLPIRMMAMECIIMGKFTTASDVAFSVTLMEVL 843
 DB 687 LLVKTIGDFGMSRDYVSTDYRVGHTMLPIRMMPEISIMYRKTTSDVMSGLVAMEIF 746
 QY 844 MCRAPQFQQLDQVYENAGFEFRQGRQVILSRPAPQGLIYELMKCSWSESQRPP 903
 DB 747 TYGK-QPMYQLSNNEVTECI---TQGR-VLQRRPTCPQEVYELMLGCMQWRPPTTRKN 798
 QY 904 FSQHLRFL 911
 DB 799 IKNIHTLL 806

RESULT 12
 S44098
 brain-derived neurotrophic factor receptor precursor - chicken
 N:Alternate names: receptor tyrosine kinase trkB
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999

C:Accession: S59939; S42175; S44098
 R:Vinh, N.O.; Erdmann, K.S.; Heumann, R.
 Gene 149, 383-384, 1994
 A:Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of
 A:Reference number: S59939; MUID:95047511
 A:Accession: S59939
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-818 <Y12>
 A:Cross-references: EMBL:X77251; NID:9563881; PIDN:CAA54468.1; PID:9472934
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 R:Dechant, G.; Biffo, S.; Okazawa, H.; Kolbeck, R.; Pottgiesser, J.; Barde, Y.A.
 Development 119, 545-550, 1993
 A:Title: Expression and binding characteristics of the BDNF receptor chick trkB.
 A:Reference number: S42175; MUID:94116452
 A:Accession: S42175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-818 <DEC>
 A:Cross-references: EMBL:X74109; NID:9407798; PIDN:CAA52210.1; PID:9407799
 C:Genetics:
 A:Gene: trkB
 C:Function:
 A:Description: regulation of nervous system development; receptor for brain-derived
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-gly
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fac
 inase

Query Match 13.1%; Score 648; DB 1; Length 818;
 Best Local Similarity 34.2%; Pred. No. 1.9e-22;
 Matches 176; Conservative 71; Mismatches 149; Indels 118; Gaps 19;

QY 446 LLSKAEKRVLEELIYH-LSVPDDTILLNNRPPRPPPTQF---PRPGNPPH----- 495
 DB 360 LLMKNEGGEDKRVDAHFMSVPGD-----GSGPIYDPDYVEETPNPDIGDTNNSNOI 413
 QY 496 SARPCEVNG-----SALLSNPARYLLATATARP---RGGPPTPAMAKP 537
 DB 414 TSPDVCKNEMEDSTYYVVGIALVCTGLVIMLLIKGRHSGFKMGKD----- 463
 QY 538 TNYQVSGDIEMPEKPGAPLPPPPQNSVPHYAEADIVTQGVGNTYAVPALPGAVG 597
 DB 464 ---SSVISND---DASAPL-----HHSNSNPTSSSGGPRDAVITGMKPIYI 507
 QY 598 DGPPRVDFPRSRK-----FKRKGEGQGEVHLC---VDSPODVLSDP 640
 DB 508 ENFOYGTINSOLKPDTEVOHNRHIVLKRLEGGAFKVFLEACVYLCEPD----- 561
 QY 641 PLNVRKGHPLVAVKILRPDATKNASFSLFSRNDPFEKVKIMSLKDPNIRLLGVCYOD 700
 DB 562 -----KIIVAVYTKL-DASDNA-----KDFHREAEELLTNLQHEHIVAFYGVCHG 606
 QY 701 DPLCMITDYMEGDIQGLSAHQLEDKAAGAPGDDQAAG---PTISYPMILHYAAQIA 757
 DB 607 DPLIMFEYMKHGDLNKLFRH-----GPDVAVLMAGNRPALITQOSMLHTAQOIA 657
 QY 758 SGMRYLATLNFVHRDLATRNCLVGENFTIKIDFGMSRLVAGDYRYVQRAVLPIRMA 817

[illegible]

	Query Match	13.18	Score 645	DB 1	Length 822
	Best Local Similarity	46.55	Pred. No. 2	6e-22	
	Matches 144	Conservative 45	Mismatches 79	Indels 42	Gaps
QY	607	RSRLTEKKEKLGEGGFEVHLC	--VDSPODVLSDLPPLVNRKGGPPLVAVKILRDPATK	6633	
		:	:		
Db	535	RHNITLKRELTEGEGAFKFKFLTECNLCPEOD	-----KIVAVKTLK-DASD	5799	
		:	:		
QY	664	NASFSLFRNDELFEVKRMSLTKDNPNIIRILGVCVODDPLCMITDYNENNDLQNFSLAHQ	7233		
		: : :	:		

[illegible]

RESULT 14
A55178
neurotrophin receptor trkC precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Jun-1999
C:Accession: A55178
R:McGregor, L.M.; Bayliss, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.
Genomics 22:267-272, 1994
A:Title: Molecular cloning of the cDNA for human trkC (NTRK3), chromosomal assignment
A:Reference number: A55178; MUID:95104834
A:Accession: A55178
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-825 <MG>
A:Cross-references: GB:005012; NID:g442389; PIDN:AAA75374.1; PID:g442390
C:Genetics:
A:Gene: GDB:NTRK3
A:Cross-references: GDB:127899; OMIM:191316
A:Map position: 15q24-15q25
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
C:Keywords: alternative splicing; ATP; growth factor receptor
F:79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical
F:156-817/Domain: protein kinase homology <KIN>
F:544-552/Region: protein kinase ATP-binding motif

Query Match	13.0%: Score 641.5; DB 2; Length 825.
Best Local Similarity	32.5%: Pred. NO.3.8e-22;
Matches 174; Conservative	67; Mismatches 133; Indels 163; Gaps 19;
QY	490 RGNPHSAPCPVNG-----SALLSNPA-----YRLLATYAR 522
DB	326 RGNPPPTLHMLHNOGPLEESKIIHVEYEOEGEISGCLLFKPTHYNNGNITLT----AK 381
QY	523 PPRGGPPTPAKMAKPTNTQAVSGDYE--PEKGPAPLL---PPPNQSVPHYAEADIV 575
DB	382 NPLG-----TANQTINGHFLKPPPESTONFLTFDEVSPPTIYVHKKEEDPE 430
QY	576 TLQGVTVGNTVAVPAL-----P 592
DB	431 GVSIAVGIAAFACVLLVLFVMIKNGRRSRFGMKGPYAVISGEEDSASPLHHNHGITT 490
QY	593 PGAVGDDG-----PRVDFP-----RSRLRFKEKLGSGGFG 622
DB	491 PSSLDAGPDIVYIGMTRLPVIEINPOYFPOGHNCHKPDITYOHIKRDVLVLRLEGEAGFG 550
QY	623 EVHLCEVDSPODVLSDLPFLNVRKGHPFLVAVKILRPDPATKNASFSLFSRNDFLKEVIM 682
DB	551 KVLFLAEC-----YNLSPTK-DKTLVAVKRLK-DPT-----LAARDPFOREALL 592
QY	683 SRLKDPNIIIRLLGVCVODDPLCMITTDYENGLDNQIFSAHOLEDKAAAGAGF---DGQ 737

Db 593 TNLHEHIVKFEYGCDDPLIMVEYMKHGDINKFLRAH-----GPNAMILVYDQ 643

QY 738 AAGP-TISYMLHVAQAISGRYATLNFVRDLATRNCLVGENFTIKIADFGSMRN 796

Db 644 PROAKGELGSLQMLHISQIASGVYLAOSHVRDLATRNCLVGENFTIKIADFGSMRD 703

QY 797 LAGDYRVAGRAVLPIFRMAMECILMGFTTASDVMAFVGLMELCRAPPGQLT 856

Db 704 VYSDYRVAGRHMTLPFRMAMECILMGFTTASDVMAFVGLMELCRAPPGQLT 762

QY 857 EGVENAGFEFFRDGROVYLSRPPACDGLYELMLRCWRSRSEORPPESQLHFL 911

Db 763 TEVIECI-----TQGR--VLERPRVCPREVYDVMLGCMQRRPQRLNKEIKYL 810

RESULT 15

TVRTTB

nerve growth factor receptor precursor, high affinity - rat

N:Alternate names: receptor tyrosine kinase trka

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 02-Jun-2000

C/Accession: A41981

R:Weakin, S.O.; Suter, U.; Drinkwater, C.C.; Welcher, A.A.; Shooter, E.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 2374-2378, 1992

A:Title: The rat trk protooncogene product exhibits properties characteristic of the src

A:Reference number: A41981, M0ID:92186121

A:Accession: A41981

A:Molecule type: mRNA

A:Residues: 1-799 <MEA>

A:Cross-reference: GB:M85214; NID:g207481; PIDN:AAA42286.1; PID:g207482

A:Note: sequence extracted from NCBI backbone (NCBI:88433, NCBI:88434)

A:Note: In Genbank entry RATTNRKPEC, release 113.0, the source is designated as Rattus r

C:Comment: The proto-oncogene trka is activated by gene fusion. The amino end of several

C:Function:

A:Description: regulation of nervous system development; receptor for nerve growth fact

C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop

C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote

C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote

C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote

F:1-33/Domain: signal sequence #status predicted <SIG>

F:33-799/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>

F:33-424/Domain: extracellular #status predicted <EXT>

F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:425-441/Domain: transmembrane #status predicted <TMN>

F:442-799/Domain: cytosolic #status predicted <CYT>

F:511-791/Domain: protein kinase homology <KIN>

F:519-527/Region: protein kinase ATP-binding motif

F:67,121,190,204,255,264,320,325,341,361,404/Binding site: carbohydrate (Asn) (covalent)

F:547/Active site: Lys #status predicted

F:683/Binding site: phosphate (Tyr) (covalent) #status predicted

F:794/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 13.0%; Score 640.5; DB 1; Length 799;

Best Local Similarity 29.5%; Pred. No. 4e-22;

Matches 190; Conservative 78; Mismatches 155; Indels 221; Gaps 22;

QY 335 SVPLGGRVARFLQC-----RFLFAGPMLLFSEISFI----- 365

Db 289 SVHLGNAVEQHHMCIPFSVDGPPAPSLRWFNGS--VLNETSFIFQFLESALTNETMRH 346

QY 366 -----SDVNNSSPALGTFP-----PAPMPGPPPTNFSSELEPR 403

Db 347 GCLRLNPTHTVNGNTLLAANPYGAASIMAAFMNDPFRFPEDPIPVSSPVDNST 406

QY 404 GQPPVAKAEGSPFALLIGLVAIILLLIILMLRMLRRLSKERR-----V 454

Db 407 SRDPVEKDETPFGVSAVGLAVSALFL-SALL-----VLNKGGRSKRGINRPV 458

QY 455 LEEF-----LTVHLSPGCTILINRPPGPREPPPTQEPFRGNPNPHSADCPVNGSAL---L 507

Db 459 LAPEDGLAMSLHFMTLGSSSL-----SPEDEKSGSLQCHI 493

QY 508 LSNPAYRLLATYAPRPPGPPPTPAKAPNTQAVSSDYMEPEKPGAPLPPPPQNSVP 567

Db 494 MENPOY-----FS-----DTCVH 506

QY 568 HYAEADIVTLGVGTGNTYAAPALPPGAVGDGPPRVDPFRSLRKEKELGSGGGEVHC 627

Db 507 HIKRQDII-----LKMELGSGAGKGVFLA 530

QY 628 E---VDSFQDLYSLDFPLNVRKGHPLVAVKILRPDARKNASFLSFRNDELKEVKIMSR 684

Db 531 ECVNMLNDQ-----KMLVAVKALK-ETSEN-----KQDFHREALLTM 569

QY 685 LKDPNIRLLGVYQDDPLCMITDYMENGDLNPLSAHQLDKAEGAPGDGQAAGPTI 744

Db 570 LQHQHIVAFEGVCTEGGFLMVFETMRHGDINRFLRSHGPPAKLLAGE--DVAPGP-L 625

QY 745 SYPMILLHVAQAISGRYATLNFVRDLATRNCLVGENFTIKIADFGSMRNLYAGDYR 804

Db 626 GLGQLLAVASQVAAQMYLASHVHVDLATRNCLVQGLVYKIGDGMSSDITSTDIYR 685

QY 805 VQGRAVLPFRMAMECILMGFTTASDVMAFVGLMELCRAPPGQLTDEGVENAG 864

Db 686 VGGRTMLPIFRMAMECILMGFTTASDVMAFVGLMELCRAPPGQLTDEGVENAG 743

QY 865 EFPDQGRVYLSRPPACDGLYELMLRCWRSRSEORPPESQLH 908

Db 744 -----TQGR--LERRPACPDVYALMGCMQRRPQRLNKEIKYL 781

Search completed: October 4, 2002, 07:41:35

Job time: 155 sec